

## CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/6/5, 285B

CRF Processing Date: 7/17/2002

Edited by: 10/1/02

Verified by: (STIC staff)

ENTERED

1642 1600 #16  
DmT  
7-26-02  
JUL 15 2002  
RECEIVED  
TECH CENTER 1600/2800

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.



## RAW SEQUENCE LISTING

DATE: 07/11/2002

PATENT APPLICATION: US/09/615,285B

TIME: 08:08:00

Input Set : N:\AMC\51158-20008.txt

Output Set: N:\CRF3\07112002\I615285B.raw

p.6

4 <110> APPLICANT: Afar, Daniel E. H.  
 5 Hubert, Rene S.  
 6 Leong, Kahan  
 7 Raitano, Arthur B.  
 8 Saffran, Douglas C.  
 9 Mitchell, Stephen C.  
 10 Jakobovits, Aya  
 11 Faris, Mary  
 12 Vivanco, Igo  
 14 <120> TITLE OF INVENTION: NOVEL TUMOR ANTIGEN USEFUL IN DIAGNOSIS  
 15 AND THERAPY OF PROSTATE AND COLON CANCER  
 18 <130> FILE REFERENCE: 511582000820  
 20 <140> CURRENT APPLICATION NUMBER: 09/615,285B  
 C--> 21 <141> CURRENT FILING DATE: 2002-06-20  
 23 <150> PRIOR APPLICATION NUMBER: 09/323,597  
 24 <151> PRIOR FILING DATE: 1999-06-01  
 26 <150> PRIOR APPLICATION NUMBER: 60/087,598  
 27 <151> PRIOR FILING DATE: 1998-06-01  
 29 <150> PRIOR APPLICATION NUMBER: 60/091,474  
 30 <151> PRIOR FILING DATE: 1998-06-29  
 32 <150> PRIOR APPLICATION NUMBER: 60/129,521  
 33 <151> PRIOR FILING DATE: 1999-04-14  
 35 <160> NUMBER OF SEQ ID NOS: 43  
 37 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 39 <210> SEQ ID NO: 1  
 40 <211> LENGTH: 1738  
 41 <212> TYPE: DNA  
 42 <213> ORGANISM: Homo sapiens  
 44 <220> FEATURE:  
 45 <221> NAME/KEY: CDS  
 46 <222> LOCATION: (112)...(1588)  
 48 <400> SEQUENCE: 1  
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 50 attgaacatt ccagatacct atcattactc gatgctgttg ataacagcaa g atg gct 117  
 51 Met Ala  
 52 1  
 54 ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac cat 165  
 55 Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn His  
 56 5 10 15  
 58 gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc ccc 213  
 59 Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val Pro  
 60 20 25 30  
 62 act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg ccc 261

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63 Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val Pro
64 35 40 45 50
66 cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc tgc 309
67 Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val Cys
68 55 60 65
70 acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act aag 357
71 Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr Lys
72 70 75 80
74 aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga gct 405
75 Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly Ala
76 85 90 95
78 gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc tcc 453
79 Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys Ser
80 100 105 110
82 aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc tct 501
83 Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser
84 115 120 125 130
86 aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag aat 549
87 Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn
88 135 140 145
90 cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag gtg tac tca 597
91 Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val Tyr Ser
92 150 155 160
94 tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac gag 645
95 Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu
96 165 170 175
98 aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat ttt 693
99 Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe
100 180 185 190
102 tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt atg 741
103 Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe Met
104 195 200 205 210
106 aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg tac 789
107 Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr
108 215 220 225
110 cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt ata 837
111 His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile
112 230 235 240
114 gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg att gtg ggc 885
115 Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly
116 245 250 255
118 ggc gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg cac 933
119 Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His
120 260 265 270
122 gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag tgg 981
123 Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu Trp
124 275 280 285 290
126 atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca tgg 1029
127 Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro Trp

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Input Set : N:\AMC\51158-20008.txt

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128          295          300          305
130 cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc tat      1077
131 His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr
132          310          315          320
134 gga gcc gga tac caa gta gaa aaa gtg att tct cat cca aat tat gac      1125
135 Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn Tyr Asp
136          325          330          335
138 tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag cct      1173
139 Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys Pro
140          340          345          350
142 ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca ggc      1221
143 Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro Gly
144 355          360          365          370
146 atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg gcc      1269
147 Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly Ala
148          375          380          385
150 acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag gtg      1317
151 Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys Val
152          390          395          400
154 ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac aac      1365
155 Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp Asn
156          405          410          415
158 ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac gtc      1413
159 Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn Val
160          420          425          430
162 gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aag aac      1461
163 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Lys Asn
164 435          440          445          450
166 aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt gcc      1509
167 Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys Ala
168          455          460          465
170 aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg gac      1557
171 Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr Asp
172          470          475          480
174 tgg att tat cga caa atg agg gca gac ggc t aatccacatg gtcttcgtcc      1608
175 Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
176          485          490
178 ttgacgtcgt tttacaagaa aacaatgggg ctggttttgc ttccccgtgc atgatttact      1668
179 cttagagatg attcagaggt cacttcattt ttattaaaca gtgaacttgt ctggcaaaaa      1728
180 aaaaaaaaaa      1738
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 492
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
187 <400> SEQUENCE: 2
188 Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
189 1          5          10          15
190 Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
191          20          25          30

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192 Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
193          35          40          45
194 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
195          50          55          60
196 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
197 65          70          75          80
198 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
199          85          90          95
200 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
201          100          105          110
202 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
203          115          120          125
204 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
205          130          135          140
206 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val
207 145          150          155          160
208 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
209          165          170          175
210 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
211          180          185          190
212 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
213          195          200          205
214 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
215          210          215          220
216 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
217 225          230          235          240
218 Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
219          245          250          255
220 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
221          260          265          270
222 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
223          275          280          285
224 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
225          290          295          300
226 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
227 305          310          315          320
228 Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn
229          325          330          335
230 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
231          340          345          350
232 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
233          355          360          365
234 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
235          370          375          380
236 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
237 385          390          395          400
238 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
239          405          410          415
240 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly

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241          420          425          430
242 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
243          435          440          445
244 Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
245          450          455          460
246 Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
247 465          470          475          480
248 Thr Asp Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
249          485          490
251 <210> SEQ ID NO: 3
252 <211> LENGTH: 2479
253 <212> TYPE: DNA
254 <213> ORGANISM: Homo sapiens
256 <220> FEATURE:
257 <221> NAME/KEY: CDS
258 <222> LOCATION: (57)...(1534)
260 <400> SEQUENCE: 3
261 gtcattattga acattccaga tacctatcat tactcgatgc tgttgataac agcaag atg      59
262                                     Met
263                                     1
265 gct ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac      107
266 Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn
267          5          10          15
269 cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc      155
270 His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val
271          20          25          30
273 ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg      203
274 Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val
275          35          40          45
277 ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc      251
278 Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val
279 50          55          60          65
281 tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act      299
282 Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr
283          70          75          80
285 aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga      347
286 Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly
287          85          90          95
289 gct gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc      395
290 Ala Ala Leu Ala Ala Gly Leu Trp Lys Phe Met Gly Ser Lys Cys
291          100          105          110
293 tcc aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc      443
294 Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro
295          115          120          125
297 tct aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag      491
298 Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu
299 130          135          140          145
301 aat cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag atg tac      539
302 Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met Tyr

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 07/11/2002  
PATENT APPLICATION:    US/09/615,285B      TIME: 08:08:01

Input Set : N:\AMC\51158-20008.txt  
Output Set: N:\CRF3\07112002\I615285B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 206,274